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OM protein - protein search, using sw model

Run on: March 24, 2003, 15:45:24 ; Search time 55.3636 Seconds
(without alignments)
628.181 Million cell updates/sec

Title: US-09-988-971-2

Perfect score: 1351
Sequence: 1 MSLPSRKSLPSPSSSV.....RESLPTSLNDEAVSIDDA 261

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database :

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1: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA1980.DAT:*
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20: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA1999.DAT:*
21: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA2000.DAT:*
22: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA2001.DAT:*
23: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA2002.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1351	100.0	261	23	AAO15457
2	1347	99.7	261	23	AAU91308
3	1273	94.2	248	21	AAAB2993
4	1032	76.4	259	23	AAO15456
5	938.5	69.5	210	23	AAO15458
6	474.5	35.1	315	22	AAU31072
7	364.5	27.0	505	22	AAAB9332
8	352	26.1	509	21	AAV49420
9	344	25.5	508	21	AAAB3700
10	342	25.3	70	22	ABG05994

11	336	24.9	517	22	ABB57957	Drosophila melanog
12	321	23.8	541	23	AAU74614	Perinuclear checa
13	319.5	23.6	543	22	ABG10302	Novel human diago
14	319.5	23.6	543	22	AAAB8463	Novel human diago
15	317.5	23.5	496	20	AAV29668	Amino acid sequenc
16	317.5	23.5	543	20	AAV24421	Human src-family k
17	314.5	23.3	496	22	AAU08730	Human yes1 protein
18	314.5	23.3	496	22	AAU08730	Xenopus laevis src
19	314.5	23.3	496	22	AAU08730	Xenopus laevis src
20	310.5	23.0	551	22	ABG22264	Novel human diago
21	290.5	21.5	533	21	AAV44447	Wild-type chicken
22	290.5	21.5	533	21	AAV44449	Mutant chicken C-S
23	290.5	21.5	533	22	AAAB8461	Amino acid sequenc
24	290.5	21.5	552	22	ABAB5777	Drosophila melanog
25	290.5	21.5	552	22	ABAB5777	Drosophila melanog
26	288.5	21.4	533	14	AAAB39705	Chicken pp60 c-src
27	286	21.2	502	23	AAE21689	Fugu rubripes lym
28	285.5	21.1	533	21	AAV44451	Mutant chicken C-S
29	280.5	20.8	536	14	AAAB39706	Human pp60 c-src p
30	280.5	20.8	536	23	AAU78678	Human SH2/SH3 doma
31	277.5	20.5	542	23	ABAB97339	Novel human protei
32	266	19.7	134	17	AAW03982	DETI1-DETI2-spacer-e
33	266	19.7	134	17	AAW02120	DETI1-DETI2-spacer-e
34	266	19.7	134	18	AAW11286	Human Ick SH2 doma
35	266	19.7	134	18	AAW11286	Human Ick SH2 doma
36	266	19.5	101	18	AAW31184	Human p56-lck prot
37	264	19.4	224	18	AAW14788	FRBP-LCK:SH2 fusio
38	262	19.4	224	20	AAW96823	A fusion protein o
39	258.5	19.1	102	16	AAW72090	Novel human diago
40	256	18.9	565	22	ABG23778	(Beta-galactosidas
41	256	18.9	565	22	ABG23778	Human src-family k
42	242	17.9	417	12	AAW14201	Src-family kinase
43	238	17.6	94	22	AAV29670	SH2 domain from hu
44	238	17.6	94	22	AAU08732	
45	237	17.5	117	17	AAW03986	

ALIGNMENTS

RESULT 1	AAO15457	standard: Protein: 261 AA.
ID	AAO15457	
XX	AAO15457:	
AC	03-OCT-2002 (first entry)	
XX		
DE	Human modulator of antigen receptor signalling (MARS) protein.	
KW	Human: gene therapy; modulator of antigen receptor signalling; MARS;	
KW	tumour suppressor gene; Src-like adaptor protein; SLAP;	
KW	myeloid malignancy; acute myelogenous leukaemia; autoimmune disorder;	
KW	immunosuppression; myeloproliferative disorder; breast cancer.	
OS	Homo sapiens.	
XX		
PN	W0200242452-A2.	
XX		
PD	30-MAY-2002.	
XX		
PF	26-NOV-2001: 2001WO-CA01662.	
XX		
PR	27-NOV-2000: 2000CA-2324663.	
XX		
PA	(HOSP-) HOSPITAL FOR SICK CHILDREN.	
XX		
PI	McGlade JC, Loreto MP;	
XX		
DR	WPI: 2002-566564/60.	
XX		
DR	N-PSDB: AAL44089.	
XX		
PT	New isolated modulator of antigen receptor signalling protein or its	

fragment, useful for treating malignant disorders such as myeloid malignancies, autoimmune disorders and myeloproliferative disorders -

Claim 7: Fig 9A: 110pp: English.

The invention comprises the amino acid and coding sequences of modulator of antigen receptor signalling (MARS) proteins. The MARS protein is a putative tumour suppressor gene and exhibits structural and sequence similarity to the ser-like adaptor protein (SLAP). The MARS DNA and protein sequences of the invention are useful for the treatment of myeloid malignancies (e.g. acute myelogenous leukaemia) autoimmune disorders, immunosuppression, myeloproliferative disorders and malignancies related to the de-regulation of tyrosine kinases (e.g. breast cancer). The present amino acid sequence represents a human MARS protein.

Sequence 261 AA:

Query Match 100.0%; Score 1351; DB 23; Length 261;
Best Local Similarity 100.0%; Pred. No. 1.7e-130;
Matches 261; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 MGSLPSRRKSLPSPSSSSVGGPGVTMEAKSKATAVAGSPAGPAELSLRGEPLT 60
1 MGSLPSRRKSLPSPSSSSVGGPGVTMEAKSKATAVAGSPAGPAELSLRGEPLT 60
1 IVSEDDGMWTVLSEVSGREYNIIPSVHAKVSHGMVLEGLSREKAEELLLPENGAFLLI 120
61 IVSEDDGMWTVLSEVSGREYNIIPSVHAKVSHGMVLEGLSREKAEELLLPENGAFLLI 120
61 IVSEDDGMWTVLSEVSGREYNIIPSVHAKVSHGMVLEGLSREKAEELLLPENGAFLLI 120
121 RESQTRRGSSYSLSVLRSPASMDRIIRHYRICHLDNGWLYISPRUTPSQALVDHYSLELA 180
121 RESQTRRGSSYSLSVLRSPASMDRIIRHYRICHLDNGWLYISPRUTPSQALVDHYSLELA 180
181 DDICCLKEPCVLOAGAPLPKGDPLPVTVQRTPLNKEELSSILSEATGESLSSEG 240
181 DDICCLKEPCVLOAGAPLPKGDPLPVTVQRTPLNKEELSSILSEATGESLSSEG 240
241 LRESLSFYISLNDENAVSLDDA 261
241 LRESLSFYISLNDENAVSLDDA 261

RESULT 2

AA091308 standard; Protein: 261 AA.

AA091308:

18-JUN-2002 (first entry)

Human protein NOV13.

Human: NOVX: gene therapy; cardiomyopathy; atherosclerosis;
cell signal processing disorder; metabolic pathway modulation disorder;
diabetes; cancer; adenocarcinoma; lymphoma; prostate cancer;
uterus cancer; immune response; graft-versus-host disease;
acquired immunodeficiency syndrome; AIDS; asthma; Crohn's disease;
hyperextension; congenital heart defects; multiple sclerosis; inflammation;
Albright hereditary osteodystrophy.

Homo sapiens.

WO200216599-A2.

28-FEB-2002.

27-AUG-2001; 2001WO-US26510.

25-AUG-2000; 2000US-228191P.

08-FEB-2001; 2001US-267300P.

20-FEB-2001; 2001US-269661P.

20-MAR-2001; 2001US-277337P.

(CURA-) CURAGEN CORP.
(CORT-) COR THERAPEUTICS INC.

Burgess CE, Conley PB, Grosse MM, Hart M, Kekuda R, Shinkets RA;
Spletter KA, Szekeres ES, Tomlinson JE, Topper JN, Yang R;

WPI: 2002-280937/32.

N-PSDB: ABK61465.

New polypeptides for treating or preventing a disorder associated with them, in humans, e.g. cardiomyopathy, atherosclerosis or cancers -
Claim 3: Page 98: 263pp: English.

The invention relates to an isolated polypeptide (NOVX) a mature form of NOVX, a NOVX variant (differing by no more than 15%), the nucleotide encoding NOVX (or its complement, fragment or variant), NOVX is NOVX-14, 15a, 15b, 16a, and 16b. The NOVX polypeptide, nucleic acid encoding it and antibody against it, are useful for treating or preventing (e.g. by gene therapy) a NOVX-associated disorder in humans, e.g. cardiomyopathy, atherosclerosis, a disorder related to cell signal processing and metabolic pathway modulation, diabetes or cancers. The NOVX polypeptide and nucleic acids are also useful for determining the presence of predisposition to the diseases. The NOVX nucleic acid and polypeptide are especially useful in therapeutic or prophylactic applications for disorders associated with aberrant NOVX expression or activity, e.g. cancers (e.g. adenocarcinoma, lymphoma, prostate cancer or uterine cancer), immune response, graft-versus-host disease, acquired immunodeficiency syndrome (AIDS), asthma, Crohn's disease, hypertension, congenital heart defects, multiple sclerosis, inflammation or Albright hereditary osteodystrophy and many other diseases listed in the specification. The DNA encoding the protein is useful in gene therapy for treating the conditions. This is also useful in detection assays, chromosome mapping, tissue typing, diagnostic or prognostic assays, or for developing a powerful assay system for functional analysis of various human disorders, as well as in diagnostic applications. The present sequence represents a NOVX protein.

Sequence 261 AA:

Query Match 99.7%; Score 1347; DB 23; Length 261;
Best Local Similarity 99.6%; Pred. No. 4.4e-130;
Matches 260; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

1 MGSLPSRRKSLPSPSSSSVGGPGVTMEAKSKATAVAGSPAGPAELSLRGEPLT 60
1 MGSLPSRRKSLPSPSSSSVGGPGVTMEAKSKATAVAGSPAGPAELSLRGEPLT 60
1 IVSEDDGMWTVLSEVSGREYNIIPSVHAKVSHGMVLEGLSREKAEELLLPENGAFLLI 120
61 IVSEDDGMWTVLSEVSGREYNIIPSVHAKVSHGMVLEGLSREKAEELLLPENGAFLLI 120
61 IVSEDDGMWTVLSEVSGREYNIIPSVHAKVSHGMVLEGLSREKAEELLLPENGAFLLI 120
121 RESQTRRGSSYSLSVLRSPASMDRIIRHYRICHLDNGWLYISPRUTPSQALVDHYSLELA 180
121 RESQTRRGSSYSLSVLRSPASMDRIIRHYRICHLDNGWLYISPRUTPSQALVDHYSLELA 180
181 DDICCLKEPCVLOAGAPLPKGDPLPVTVQRTPLNKEELSSILSEATGESLSSEG 240
181 DDICCLKEPCVLOAGAPLPKGDPLPVTVQRTPLNKEELSSILSEATGESLSSEG 240
241 LRESLSFYISLNDENAVSLDDA 261
241 LRESLSFYISLNDENAVSLDDA 261

RESULT 3

AA042993 standard; Protein: 248 AA.

AA042993:

08-FEB-2001 (first entry)

Human ORFX ORF2757 polypeptide sequence SEQ ID NO:5514.

Human: open reading frame: ORFX: detection; cytostatic; hepatotropic; vulnereary; antiproliferative; antiparkinsonian; neurotropic; neuroprotective; anticonvulsant; osteopathic; antitumor; immunosuppressant; cardiac; immunostimulant; thrombolytic; coagulant; vasotropic; antidiabetic; hypotensive; dermatological; immunosuppressive; antineoplastic; antiviral; antibacterial; antifungal; antirheumatic; antithyroid; antinaeemic; gene therapy; cancer; proliferative disorder; hypertension; neurodegenerative disorder; osteoarthritis; graft vs host disease; cardiovascular disease; diabetes mellitus; hypothyroidism; SCID; AIDS; cholesterol ester storage; systemic lupus erythematosus; infection; severe combined immunodeficiency; malaria; autoimmune disorder; asthma; allergy; aplastic anaemia; nocturnal haemoglobinuria; burn; wound; bone damage; cartilage damage; antineoplastic disease; coagulation; thrombosis; contraceptive.

Homo sapiens.

MO200058473-A2.

05-OCT-2000.

31-MAR-2000; 2000MO-US08621.

31-MAR-1999; 99US-0127607.

02-APR-1999; 99US-0127636.

05-APR-1999; 99US-0127728.

30-MAR-2000; 2000US-0540763.

(CURA-) CURAGEN CORP.

Shimkels RA, Leach M;

WPI: 2000-602362/57.

N-PSDB; AAC77202.

Novel nucleic acids and peptides derived from open reading frame X,

useful for treating e.g. cancers, proliferative disorders,

neurodegenerative disorders and cardiovascular disease.

Claim 11: Page 4693-4694; 5507pp; English.

AAC74446 to AAC77606 encode the proteins given in AAB0337 to AAB43397, which represent the human ORFX open reading frames 1 to 3161. The ORFX sequences have activities such as: cytostatic; hepatotropic; vulnereary; antiproliferative; antiparkinsonian; neurotropic; neuroprotective; anticonvulsant; osteopathic; antitumor; immunosuppressant; immunostimulant; cardiac; thrombolytic; coagulant; vasotropic; antidiabetic; hypotensive; dermatological; immunosuppressive; antineoplastic; antirheumatic; antithyroid; antinaeemic; gene therapy; cancer; proliferative disorder; hypertension; neurodegenerative disorder; osteoarthritis; graft vs host disease; cardiovascular disease; diabetes mellitus; hypothyroidism; hypothyroidism; cholesterol ester storage; systemic lupus erythematosus; severe combined immunodeficiency (SCID); AIDS; viral, bacterial or fungal infection, malaria, autoimmune disorders, asthma, allergies, aplastic anaemia, burns, wounds, bone and cartilage damage, nocturnal haemoglobinuria, antineoplastic disease; coagulation; thrombosis; and as a contraceptive.

Sequence 248 AA;

Query Match 94.2%; Score 1273; DB 21; Length 248;

Best Local Similarity 99.2%; Pred. No. 1.7e-122;

Matches 245; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

15 SLSSVQGGGPTWAEARSKATVAALGSPAGPAELSLRGLPELTIVSEDDGMWTVLSE 74

DB 2 SLSSVQGGGPTWAEARSKATVAALGSPAGPAELSLRGLPELTIVSEDDGMWTVLSE 61

QY 75 VSGREYNIPDVHAKVSHGWLVEGLSREKAEELLPLGNGAFILRSQTRRGSYSLSV 134

DB 62 VSGREYNIPDVHAKVSHGWLVEGLSREKAEELLPLGNGAFILRSQTRRGSYSLSV 121

QY 135 RLSRPSMRIRHRIHCLDNGWLYSPRLTPPSLOLVDPHSELAADICCLKEPVQ 194

DB 122 RLSRPSMRIRHRIHCLDNGWLYSPRLTPPSLOLVDPHSELAADICCLKEPVQ 181

QY 195 RAGPLFGKTIPLPYVOTRPLMKNKELDSLSFSEATGEESSLBSGLRSYFYSUNDE 254

DB 182 RAGPLFGKTIPLPYVOTRPLMKNKELDSLSFSEATGEESSLBSGLRSYFYSUNDE 241

QY 255 AVSLDDA 261

DB 242 AVSLDDA 248

RESULT 4

AA015456

ID AA015456 standard; Protein; 259 AA.

AA015456;

03-OCT-2002 (first entry)

Mouse modulator of antigen receptor signalling (MARS) protein.

Mouse; gene therapy; modulator of antigen receptor signalling; MARS;

tumour suppressor gene; scr-like adaptor protein; SLAP;

myeloid malignancy; acute myelogenous leukaemia; autoimmune disorder;

immunosuppression; myeloproliferative disorder; breast cancer.

Mus sp.

MO200242452-A2.

30-MAY-2002.

26-NOV-2001; 2001MO-CA01662.

27-NOV-2000; 2000CA-2324663.

(HOSP-) HOSPITAL FOR SICK CHILDREN.

McGlade JC, Loreto MP;

WPI: 2002-566564/60.

N-PSDB; AAL44087.

New isolated modulator of antigen receptor signalling protein or its

fragment, useful for treating malignant disorders such as myeloid

malignancies, autoimmune disorders and myeloproliferative disorders

Claim 7; Fig 1A; 110pp; English.

The invention comprises the amino acid and coding sequences of modulator

of antigen receptor signalling (MARS) proteins. The MARS protein is a

putative tumour suppressor gene and exhibits structural and sequence

similarity to the Scr-like adaptor protein (SLAP). The MARS DNA and

protein sequences of the invention are useful for the treatment of

myeloid malignancies (e.g. acute myelogenous leukaemia) autoimmune

disorders, immunosuppression, myeloproliferative disorders and

malignancies related to the de-regulation of tyrosine kinases (e.g.

breast cancer). The present amino acid sequence represents a mouse MARS

protein.

Sequence 259 AA;

Query Match 76.4%; Score 1032; DB 23; Length 259;

Best Local Similarity 79.8%; Pred. No. 1.2e-97;

Matches 209; Conservative 16; Mismatches 33; Indels 4; Gaps 3;

QY 1 MGSLPSRRKSLSPSPSLSSVQGGPVTMEAKRSKATVALGSPAGPAELSLRLGEPLT 60
 1 MGSLSSSKGT-SSPSSSSGPDQEPVSMQPERHKKVTVAAGSPAGEQARLSRLRGEP 59
 DB 61 IVSEDDGMWTVLSEVSGREYNIPSVHVAVSHGMLYEGLSREKAEELLLPENGGAFLI 120
 60 IISDGDMMTVLSEVSGREYHMFSSVYAAVANGMLYEGLSREKAEELLLPENGGAFLI 119
 QY 121 RESQTRRGYSLSVRLSPASMDRIRHRYRICHLDNGMLYISPLTFPSIQALVDHYSELA 180
 120 RESQTRRGYSLSVRLSPASMDRIRHRYRICHLDNGMLYISPLTFPSIQALVDHYSELA 179
 DB 181 DDICCLKEPCVQIRAGPPLPKDIPLVTVORTPLNMKEELSSILFSEA-ATGEESLSE 239
 180 DGICCPREPVCYLKGLPRLPKDTPPPVPTSSLNKKKDRSLLEAPASGASLSLSE 239
 QY 240 GLRESLSFYISLNDKAVSLDDA 261
 DB 240 GLRESLSFYISLNDKAVSLDDA 261
 DB 240 GLRESLSFYISLNDKAVSLDDA 261

RESULT 5
 AA015458
 ID AA015458 standard: Protein; 210 AA.

AC AA015458:
 XX
 XX
 DT 03-OCT-2002 (first entry)
 XX
 XX
 DE Mouse modulator of antigen receptor signalling short isoform protein.
 XX
 XX Mouse; gene therapy: modulator of antigen receptor signalling; MARS;
 KM tumour suppressor gene; Scr-like adaptor protein; SLAP;
 KM myeloid malignancy; acute myelogenous leukemia; autoimmune disorder;
 KM immunosuppression; myeloproliferative disorder; breast cancer.
 XX
 OS Mus sp.
 XX
 PN W0200242452-A2.
 XX
 PD 30-MAY-2002.
 XX
 PF 26-NOV-2001; 2001WO-CA01662.
 XX
 PR 27-NOV-2000; 2000CA-2324663.
 XX
 PA (HOSP-) HOSPITAL FOR SICK CHILDREN.
 XX
 PI Mcglade JC, Loreto MP;
 XX
 DR WPI: 2002-566564/60.
 DR N-PSDB; AAL44090.
 XX
 XX New isolated modulator of antigen receptor signalling protein or its
 PT fragment, useful for treating malignant disorders such as myeloid
 PT malignancies, autoimmune disorders and myeloproliferative disorders -
 XX
 PS Claim 8; Page 78; 110pp: English.

XX The invention comprises the amino acid and coding sequences of modulator
 CC of antigen receptor signalling (MARS) proteins. The MARS protein is a
 CC putative tumour suppressor gene and exhibits structural and sequence
 CC similarity to the Scr-like adaptor protein (SLAP). The MARS DNA and
 CC protein sequences of the invention are useful for the treatment of
 CC myeloid malignancies (e.g. acute myelogenous leukemia) autoimmune
 CC disorders, immunosuppression, myeloproliferative disorders and
 CC malignancies related to the de-regulation of tyrosine kinases (e.g.
 CC breast cancer). The present amino acid sequence represents a mouse MARS
 CC protein.
 XX Sequence 210 AA;

Query Match 69.5%; Score 938.5; DB 23; Length 210;
 Best Local Similarity 89.4%; Pred. No. 3.7e-88;
 Matches 185; Conservative 3; Mismatches 12; Indels 7; Gaps 1;

QY 1 MGSLPSRRKSLSPSPSLSSVQGGPVTMEAKRSKATVALGSPAGPAELSLRLGEPLT 60
 1 MGSLPSRRKSLSPSPSLSSVQGGPVTMEAKRSKATVALGSPAGPAELSLRLGEPLT 60
 DB 61 IVSEDDGMWTVLSEVSGREYNIPSVHVAVSHGMLYEGLSREKAEELLLPENGGAFLI 120
 60 IISDGDMMTVLSEVSGREYHMFSSVYAAVANGMLYEGLSREKAEELLLPENGGAFLI 120
 QY 121 RESQTRRGYSLSVRLSPASMDRIRHRYRICHLDNGMLYISPLTFPSIQALVDHYSELA 180
 120 RESQTRRGYSLSVRLSPASMDRIRHRYRICHLDNGMLYISPLTFPSIQALVDHYSELA 178
 DB 121 RESQTRRGYSLSVRLSPASMDRIRHRYRICHLDNGMLYISPLTFPSIQALVDHYSELA 180
 121 RESQTRRGYSLSVRLSPASMDRIRHRYRICHLDNGMLYISPLTFPSIQALVDHYSELA 180
 QY 179 -----LADDICCLKEPCVQIRAGPPLP 200
 DB 181 PAPWQGYPTPCDCAEDPTQLERAGQLP 207

RESULT 6
 AAU31072
 ID AAU31072 standard: Protein; 315 AA.

AC AAU31072:
 XX
 XX
 DT 18-DEC-2001 (first entry)
 XX
 XX
 DE Novel human secreted protein #1563.
 XX
 XX Human; vaccination; gene therapy: nutritional supplement;
 KM stem cell proliferation; haematopoiesis; nerve tissue regeneration;
 KM immune suppression; immune stimulation; anti-inflammatory; leukemia.
 XX
 OS Homo sapiens.
 XX
 PN W0200179449-A2.
 XX
 PD 25-OCT-2001.
 XX
 PF 16-APR-2001; 2001WO-US08656.
 XX
 PR 18-APR-2000; 2000US-0552929.
 PR 26-JAN-2001; 2001US-0770160.
 XX
 PA (HYSE-) HYSEQ INC.
 XX
 PI Tang YT, Liu C, Drmanac RT;
 XX
 DR WPI: 2001-611725/70.
 XX
 XX Nucleic acids encoding a range of human polypeptides, useful in genetic
 PT vaccination, testing and therapy -
 XX
 PS Claim 20; Page 399; 765pp: English.

XX The invention relates to novel human secreted polypeptides. The
 CC polypeptides and antibodies to the polypeptides are useful for
 CC determining the presence of or predisposition to a disease associated
 CC with altered levels of polypeptide. The polypeptides are also useful for
 CC identifying agents (agonists and antagonists) that bind to them. Cells
 CC expressing the proteins are useful for identifying a therapeutic agent
 CC for use in treatment of a pathology related to aberrant expression or
 CC physiological interactions of the polypeptide. Vectors comprising
 CC the nucleic acids encoding the polypeptides and cells genetically
 CC engineered to express them are also useful for producing the proteins.
 CC The proteins are useful in genetic vaccination, testing and
 CC therapy, and can be used as nutritional supplements. They may be used to
 CC increase stem cell proliferation; to regulate haematopoiesis; and in
 CC bone, cartilage, tendon and/or nerve tissue growth or regeneration;
 CC immune suppression and/or stimulation; as anti-inflammatory agents; and

CC in treatment of leukaemias. AAU29510-AAU33304 represent the amino acid
 CC sequences of novel human secreted proteins of the invention.

XX Sequence 315 AA:

Query Match 35.1%; Score 474.5; DB 22; Length 315;
 Best Local Similarity 39.7%; Pred. No. 4.2e-40;

Matches 104; Conservative 46; Mismatches 99; Indels 13; Gaps 4;

QY 5 PSRRKSLPSPSLSSVQGGPYTMEAKSKATANAAGSPAGGPAELSLRGEPLTVSE 64
 DB 33 PGKKEMGMSKTPAPAEKRLPNPGCLDSDFLAVLDYSPDISPFRGKEKRLVSD 92
 QY 65 DGDMTVLSEVSGREYNIPSVHAKVSHG-WLYEGLSREKAEELLIPGNNGAGFLRES 123
 DB 93 EGGMMKAISLTGREGSYIPGICVARYHGLMFEGLRDKAEELLDLPRTKVGSMFRES 152
 QY 124 QTRRGYSLSVRLSRPASMDRIRHRIHCLDNGMLYISPRLPFSIQALVDHYSELADDI 183
 DB 153 ETKKGFYSLSVR-----HROVKTIRIFRLPNMNYISPRLPFOCLELDVNHSEVADGL 206
 QY 184 CCLLKEPCVLRAGPLPGKDIPLYTVQRTPLNKKELDSLEFSEATAGE-----ESLIS 238
 DB 207 CCVLTPTCLQSTAPAPAVRACSSPYTLRQKTVDMRRV-SRLQDEPGTENPLGVVESTLS 265
 QY 239 EGLRESLFSYISLNDVAVSLDD 260
 DB 266 YGLRESIASYLSLTSEDISSED 287

RESULT 7

AAAB99332 standard; Protein: 505 AA.

AC AAB99332;

DT 23-AUG-2001 (first entry)

XX Human tyrosine kinase Hck protein sequence SHQ ID NO.11.

XX Human: tyrosine kinase Hck binding protein: tyrosine kinase; Hck;

KW tumour lethal factor; tumour necrosis factor alpha; apoptosis; HSB-1;

KM Hck signal transduction; human immunodeficiency virus; HIV infection;

XX antileukemia.

XX Homo sapiens.

XX MO200132869-A1.

XX 10-MAY-2001.

XX 26-OCT-2000; 2000NO-JP07500.

XX 29-OCT-1999; 99JP-0309957.

XX (SSSE) SSP CO LTD.

XX Tanlyama T, Narita T;

XX WPI; 2001-316440/33.

XX New proteins which bind to human tyrosine kinase Hck for promotion of

XX apoptosis and for the elucidation of the mechanism of Hck signal

XX transduction

XX Example 1; Page 33-35; 45pp; Japanese.

XX The present invention describes a protein, designated HSB-1, which binds

XX to human tyrosine kinase Hck. Also described are: (1) nucleic acids

XX encoding the protein and its derivatives; (2) recombinant vectors

XX containing the nucleic acids; and (3) host cells transformed by the

XX vectors and expressing the protein. HSB-1 has cytosolic activity, binds

CC apoptosis. HSB-1 proteins are used for the elucidation of the mechanism
 CC of Hck signal transduction and of the role of Hck in human
 CC immunodeficiency virus (HIV) infection. They can be used for the
 CC treatment of infections and other diseases with which Hck is associated.
 CC They promote the anticancer activity of tumour necrosis factor alpha.
 CC The present sequence represents the human tyrosine kinase Hck protein,
 CC which is used in an example from the present invention.

XX Sequence 505 AA:

Query Match 27.0%; Score 364.5; DB 22; Length 505;
 Best Local Similarity 42.2%; Pred. No. 1.9e-28;

Matches 78; Conservative 31; Mismatches 69; Indels 7; Gaps 2;

QY 12 PPSLSVSSVQGGPYTMEAKSKATANAAGSPAGGPAELSLRGEPLTVSEDDGMWTV 71
 DB 40 PGFNSHNS---NTPGIREAGSEDIIVVALYVEAIIHEDISFQKDDQWVLEESGEMKA 96
 QY 72 LSEVSGREYNIPSVHAKV-----SHQWLYEGLSREKAEELLIPGNPGARLPRESQTR 127
 DB 97 RSLATRKEGYIPSNVYVARVDSLETETEFKGISKKAERQLAPENMLGSPFMRDSETK 156
 QY 128 GSTISLSVRLSRPASMDRIRHRIHCLDNGMLYISPRLPFSIQALVDHYSELADICLL 187
 DB 157 GSYSLSVRDYPDROGDTVKHKYIKRLDNGGFYISPRSTESTIQELVDHYKKGNGLCOKL 216
 QY 188 KEPCV 192
 DB 217 SVPCM 221

RESULT 8

AAV49420 standard; Protein: 509 AA.

AC AAV49420;

DT 13-MAR-2000 (first entry)

XX PKA substrate, Src-family protein.

XX Protein kinase A: PKA; PKA signaling pathway; phosphorylation; cancer;

KW kinase substrate; immunosuppressive disorder; proliferative disease;

KM HIV infection; AIDS; immunodeficiency; autoimmune disease;

XX systemic lupus erythematosus; Src-family.

XX Homo sapiens.

XX WO962315-A2.

XX 02-DEC-1999.

XX 27-MAY-1999; 99WO-GB01680.

XX 27-MAY-1998; 98NO-0002419.

XX 30-DEC-1998; 98US-0114240.

XX (LAUR-) LAURAS AS.

XX (JONES) JONES E L.

XX Hanson V, Levy FO, Mustelin T, Skalhogg BS, Sundvold V, Tasken K;

XX Wang T, Altman A, Munshi A;

XX N-PSDB; AA246491.

XX WPI; 2000-086801/07.

XX Altering the activity of protein kinase signaling pathways, used for

XX treating immunosuppressive disorders, e.g. AIDS, proliferative

XX disorders, e.g. cancers or autoimmune diseases

XX Claim 23; Page 95-96; 11pp; English.

The invention provides a novel method of altering the activity of the

CC protein kinase A (PKA) signaling pathway in a cell that comprises
 CC altering the extent of phosphorylation of one or more PKA substrates, or
 CC kinase substrates downstream in the PKA signaling pathway. Pharmaceutical
 CC substrates containing a nucleic acid molecule that encodes a PKA
 CC substrate, or fragment, precursor or functionally equivalent variant,
 CC where the sequence is modified to alter its susceptibility to
 CC phosphorylation by PKA can be used for treating a disorder exhibiting
 CC abnormal PKA signaling activity, immunosuppressive disorders or
 CC proliferative diseases. They can be used for treating e.g. HIV
 CC infection, AIDS, common variable immunodeficiency or cancers. Conditions
 CC in which upregulation of the PKA pathway is required, such as autoimmune
 CC disease, e.g. systemic lupus erythematosus, may also be treated. The
 CC present sequence represents a PKA substrate, wherein the substrate is in
 CC the Src-family, preferably Lck, Fyn, Src, Yes, Fgr, Lyn, Hck Blk, Yrk,
 CC c-Kit, Fyk, Src-1 or Src-2.

Sequence 509 AA:

Query Match 26.1%; Score 352; DB 21; Length 509;

Best Local Similarity 41.7%; Pred. No. 3.6e-27;

Matches 75; Conservative 26; Mismatches 69; Indels 10; Gaps 2;

QY 26 VTMEARSKAT-----AVALGSPAGPAELSLRLGEPLTIVSEGDGMWTVLSEVSGRE 79
 DB 49 VTTEGSPNPASPLQDNLVIALHSYEPHSDGDLGEKGEQRLLEQSGEMWKAQSLTTGOE 108
 QY 80 YNIPSVHAKVS---HGWLVEGLSREKAEELLLPGNPGAFILRESQTRGSGYSLSVR 135
 DB 109 GFIPFNFAKANSLEPEWFEFKLSRKDAERQLAPGNTHGSFLIRESESTAGSFSLSVR 168
 QY 136 LSRPASMDRIHRYRHCLDNGMLYISPRLTPEPSQALVDHYSLEADICCLKEPCVLQR 195
 DB 169 DFDONOGVEVVKHYKIRNLNDNGFYISPRITFPGLHLYRHYTNASDGLCTRLSPCQOTK 228

RESULT 9

AAB37700

ID AAB37700 standard; protein; 508 AA.

AC AAB37700;

DT 02-MAR-2001 (first entry)

DE Human lymphocyte kinase.

KW Human lymphocyte kinase; protein co-ordinate data; Lck; crystal.

OS Homo sapiens.

PN W0200070030-A1.

PD 23-NOV-2000.

PF 19-MAY-2000; 2000MO-US13881.

PR 19-MAY-1999; 99US-0134965.

PA (KINE-) KINETIX PHARM INC.

PI Zhu X;

DR WPI; 2000-68708/67.

PT Crystal of a protein-ligand complex for identifying kinase inhibitors,

PT comprises a truncated lymphocyte kinase and a ligand, and diffracts

PT X-rays to determine atomic coordinates at a resolution greater than 5

XX angstroms

PS Claim 1; Page 434-5; 438pp; English.

CC The present invention relates to a crystal of a protein-ligand complex

CC comprising a truncated lymphocyte kinase (Lck) and a ligand. The crystal

CC diffracts X-rays so that the atomic coordinates of the protein-ligand

CC complex can be determined to a resolution of greater than 5.0 Angstroms.
 CC The truncated Lck used in the present invention comprises the globular
 CC core of the corresponding full-length Lck. The present sequence is the
 CC full-length human Lck protein. The crystal of the present invention may
 CC be used to identify kinase inhibitors in screening assays, in drug
 CC screening and drug design processes, to design, select or test inhibitors
 CC of kinase enzymes, where the inhibitors are used as therapeutics for the
 CC treatment and modulation of diseases, disease symptoms or the effect of
 CC other physiological events mediated by kinases, having one or more kinase
 CC enzymes involved in their pathology.

Sequence 508 AA:

Query Match 25.5%; Score 344; DB 21; Length 508;

Best Local Similarity 41.1%; Pred. No. 2.4e-26;

Matches 74; Conservative 26; Mismatches 70; Indels 10; Gaps 2;

QY 26 VTMEARSKAT-----AVALGSPAGPAELSLRLGEPLTIVSEGDGMWTVLSEVSGRE 79
 DB 48 VTTEGSPNPASPLQDNLVIALHSYEPHSDGDLGEKGEQRLLEQSGEMWKAQSLTTGOE 107
 QY 80 YNIPSVHAKVS---HGWLVEGLSREKAEELLLPGNPGAFILRESQTRGSGYSLSVR 135
 DB 108 GFIPFNFAKANSLEPEWFEFKLSRKDAERQLAPGNTHGSFLIRESESTAGSFSLSVR 167
 QY 136 LSRPASMDRIHRYRHCLDNGMLYISPRLTPEPSQALVDHYSLEADICCLKEPCVLQR 195
 DB 168 DFDONOGVEVVKHYKIRNLNDNGFYISPRITFPGLHLYRHYTNASDGLCTRLSPCQOTK 227

RESULT 10

ABG05994

ID ABG05994 standard; Protein; 70 AA.

AC ABG05994;

DT 13-FEB-2002 (first entry)

DE Novel human diagnostic protein #5985.

KW Human: chromosome mapping; gene mapping; gene therapy; forensic;

KW food supplement; medical imaging; diagnostic; genetic disorder.

OS Homo sapiens.

PN W0200175067-A2.

PD 11-OCT-2001.

PF 30-MAR-2001; 2001MO-US08631.

PR 31-MAR-2000; 2000US-0540217.

PR 23-AUG-2000; 2000US-0649167.

PA (HYSE-) HYSEQ INC.

PI Drmanac RT, Liu C, Tang YT;

DR WPI; 2001-639362/73.

DR N-PSDB; AAS70181.

PT New isolated polynucleotide and encoded polypeptides, useful in

PT diagnostics, forensics, gene mapping, identification of mutations

PT responsible for genetic disorders or other traits and to assess

PT biodiversity

PS Claim 20; SEQ ID NO 36353; 103pp; English.

CC The invention relates to isolated polynucleotide (I) and

CC polypeptide (II) sequences. (I) is useful as hybridisation probes,

CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome

CC and gene mapping, and in recombinant production of (II). The

CC polynucleotides are also used in diagnostics as expressed sequence tags

CC for identifying expressed genes. (I) is useful in gene therapy techniques
 CC to restore normal activity of (II) or to treat disease states involving
 CC (II). (II) is useful for generating antibodies against it, detecting or
 CC quantitating a polypeptide in tissue, as molecular weight markers and as
 CC a food supplement. (II) and its binding partners are useful in medical
 CC imaging of sites expressing (II). (I) and (II) are useful for treating
 CC disorders involving aberrant protein expression or biological activity.
 CC The polypeptide and polynucleotide sequences have applications in
 CC diagnostics, forensics, gene mapping, identification of mutations
 CC responsible for genetic disorders or other traits to assess biodiversity
 CC and to produce other types of data and products dependent on DNA and
 CC amino acid sequences. ABG00010-ABG30377 represent novel human
 CC diagnostic amino acid sequences of the invention.
 CC Note: The sequence data for this patent did not appear in the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequences.

XX Sequence 70 AA:

Query Match 25.3%; Score 342; DB 22; Length 70;
 Best Local Similarity 98.5%; Pred. No. 1.8e-27;
 Matches 64; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 63 SEGDMMWTVLSEVSGREYNIPSVHAKVSHGWLKGLSREKAEELLFPNGGAFILRE 122
 DB 6 SKDGMWTVLSEVSGREYNIPSVHAKVSHGWLKGLSREKAEELLFPNGGAFILRE 65

QY 123 SQTRR 127
 DB 66 SQTRR 70

RESULT 11

ABB57957 ID ABB57957 standard; Protein; 517 AA.

XX ABB57957;

DT 26-MAR-2002 (first entry)

DE Drosophila melanogaster polypeptide SEQ ID NO 663.

KM Drosophila: developmental biology; cell signalling; insecticide;
 pharmaceutical.

OS Drosophila melanogaster.

PN WO200171042-A2.

PD 27-SEP-2001.

PF 23-MAR-2001; 2001WO-US09231.

PR 23-MAR-2000; 2000US-191637P.

PR 11-JUL-2000; 2000US-0614150.

PA (PEKE) PE CORP NY.

PI Venter JC, Adams M, Li PMD, Myers EW;

DR WPI; 2001-656860/75.

DR N-PSDB; ABL02060.

PT New isolated nucleic acid detection reagent for detecting 1000 or more
 PT genes from Drosophila and for elucidating cell signalling and cell-cell
 PT interactions -

PS Disclosure; SEQ ID NO 663; 21pp + Sequence Listing; English.

XX The invention relates to an isolated nucleic acid detection reagent
 CC capable of detecting 1000 or more genes from Drosophila. The invention is
 CC useful in developmental biology and in elucidating cell signalling and
 CC cell-cell interactions in higher eukaryotes for the development of

CC insecticides, therapeutics and pharmaceutical drugs. The invention
 CC discloses genomic DNA sequences (AB161716-AB130511), expressed DNA
 CC sequences (AB01840-AB16175) and the encoded proteins
 CC (ABB57737-ABB12072).
 CC The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequences.

XX Sequence 517 AA:

Query Match 24.9%; Score 336; DB 22; Length 517;
 Best Local Similarity 36.0%; Pred. No. 1.7e-25;
 Matches 95; Conservative 38; Mismatches 79; Indels 38; Gaps 9;

QY 11 LPSPSLSSVOCQGPVTM-----EAKSKATA---VALGSPAGGAPGLSLRLEPLT 60
 DB 36 IPMSHA-----GPPQLRPVPOIPESFAGANAKIFVALYDARDTDEDSFKRGHLE 91

QY 61 IVSE-DGDMWTVLSEVSGREYNIPSVHAKV-----SHGWLKGLSREKAEELLFPNGG 115
 DB 92 ILNDTQDGLARSKTRSGYIPSNVAKLSIAEAEWYFRKIRIKIEKKLLPENEH 151

QY 116 GAFILRESQTRRGYSYLSVRLSRPASMDRIHRYHICIDNGWLYTSPRLTSPSLQALVDH 175
 DB 152 GAFILRDSERHNDYSLSVR-----DGYVKNYRIPLDGGGFARPTFTQDELVEH 206

QY 176 YSELADIDICLLKEPCVQLRAGPLPGKDIPLPVT---VQTPPLMKELDSSLF-SEAT 231
 DB 207 YSKDSGLCWNLCRCV-----QTEKVTYEGLSHRTRODMWIDRTSLKFRKLGS 256

QY 232 GEESLSLEGL 241
 DB 257 GQFGDWEGL 266

RESULT 12

AU74614 ID AU74614 standard; Protein; 541 AA.

XX AU74614;

DT 09-APR-2002 (first entry)

DE Perinuclear theca 32 (PT32) associated tyrosine kinase, c-Yes.

KM Perinuclear theca 32; PT32; contraceptive; fertility;
 KM oocyte activation; vaccine; globozoospermy; spermiogenesis;
 KM spermatozoa; tyrosine kinase; c-Yes; immun contraceptive;
 KM bovine; protein.

OS Bos sp.

PN WO200190185-A2.

PD 29-NOV-2001.

PF 25-MAY-2001; 2001WO-CA00738.

PR 25-MAY-2000; 2000CA-2307128.

PR 25-MAY-2000; 2000US-206979P.

PA (TQOH) UNIV QUEENS KINGSTON,
 PA (UYOR-) UNIV OREGON HEALTH SCI.

PI Oko R, Sutovsky P;

DR WPI; 2002-097644/13.

DR Isolated perinuclear theca 32 polypeptide that interacts with activated
 PT tyrosine kinase c-Yes, for enhancing fertility, treating/diagnosing
 PT diminished fertility and abnormal spermiogenesis and for providing
 PT contraception -

XX

PS Example: Fig 10; 103pp; English.

XX The invention describes an isolated perinuclear theca 32 (P732)
 CC polypeptide (I) which interacts with tyrosine kinase c-yes. (I) is
 CC useful for: enhancing fertility in a mammal; treating globozoospermy, by
 CC expressing (II) in spermatozoa; inhibiting fertilisation, by introducing
 CC (I) or its antigenic fragment into a mammal to elicit an immune
 CC response; enhancing the ability of round spermatids to activate oocytes;
 CC treating or diagnosing diminished fertility and abnormal spermatogenesis;
 CC in providing contraception; identifying contraceptive and
 CC fertility-enhancing agents. The polynucleotide is useful for producing
 CC (I) by recombinant techniques, as vaccine, as diagnostic reagents, and
 CC for chromosome identification. An antibody against (I) is useful in
 CC immunological assays, in immunoneutralization methods, to identify cells
 CC expressing (I), and to purify (I) by affinity chromatography. A
 CC transgenic animal is useful as an animal model for studying human
 CC fertility and reproductive biology, and for screening compounds to
 CC identify modulators of oocyte activation. The use of (I) prevents the
 CC entry of components which are detrimental to embryonic development into
 CC the oocyte during oocyte activation with crude sperm extract and avoids
 CC the propagation of viruses such as HIV (human immunodeficiency virus) and
 CC SIV (simian immunodeficiency virus) carried in the sperm. This is the
 CC amino acid sequence of the src tyrosine kinase c-yes which is naturally
 CC occurring in sperm perinuclear theca and important in development,
 CC described in the method of the invention.

XX Sequence 541 AA;

XX Query Match 23.8%; Score 321; DB 23; Length 541;

XX Best Local Similarity 31.8%; Pred. No. 6.2e-24;

XX Matches 92; Conservative 43; Mismatches 104; Indels 50; Gaps 9;

QY 2 GSPSRKSLSPSSSSSSGCGVPTMEARSKATAVAGSPGPAELSLRLEPPLTI 61
 DB 70 GCASSFSNAPSPSPYL---GGVTV-----FVALYVKEARTDDLSKKEERQI 118
 QY 62 VSE-DGDMWTVLSEVSGREYIPSVHAKV---SHGWLVEGLSREKAEELLPGNPG 116
 DB 119 INNEGDMWEARSIATGKTYIPSNVYAPADSIOAEVYFCKMKRKAERLLNGNORG 178
 QY 117 AFLRESQTRGSGYSVLRSPASMDRIR-----HYRIHLDNGMLYISPRITPSSIOA 171
 DB 179 LEIVRESEITKGVSLSTR-----DMDEVNGDMVVKHKLRLDNGYITTRAGRESLQK 233
 QY 172 LVDRHSELADDTICLKEPC-----VLORAGPLFGKDIPLPYVQV----- 212
 DB 234 LVKHYREHADGICLHKLTVCPYVAPQTOGLAKDAWELPRESLRLEVYLGCGCEGYVMGT 293
 QY 213 ---TPLNKELDSSLSEEAATGEESLSEGLRESL-SFYISLNDNAV 256
 DB 294 WNGTTKVAITKLKPGTMMPEAFLOEQIMKKLKHKLPLVAVVSEPI 342

RESULT 13

ABG10302 standard; Protein: 543 AA.

AC ABG10302;

DT 13-FEB-2002 (first entry)

DE Novel human diagnostic protein #10293.

KW Human; chromosome mapping; gene mapping; gene therapy; forensic;

KW food supplement; medical imaging; diagnostic; genetic disorder.

OS Homo sapiens.

PN WO200175067-A2.

PD 11-OCT-2001.

PF 30-MAR-2001; 2001WO-US08631.

XX 31-MAR-2000; 2000US-0540217.
 PR 23-AUG-2000; 2000US-0649167.
 PA (HYSE-) HYSBO INC.
 XX Drmanac RT, Liu C, Tang YF;
 DR WPI: 2001-639362/73.
 DR N-PSDB; AAS74489.

PT New isolated polynucleotide and encoded polypeptides, useful in
 PT diagnostics, forensics, gene mapping, identification of mutations
 PT responsible for genetic disorders or other traits and to assess
 PT biodiversity -

PS Claim 20; SEQ ID No 40661; 103pp; English.

XX The invention relates to isolated polynucleotide (I) and
 CC polypeptide (II) sequences. (I) is useful as hybridisation probes,
 CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome
 CC and gene mapping, and in recombinant production of (II). The
 CC polynucleotides are also used in diagnostics as expressed sequence tags
 CC for identifying expressed genes. (I) is useful in gene therapy techniques
 CC to restore normal activity of (II) or to treat disease states involving
 CC (II). (II) is useful for generating antibodies against it, detecting or
 CC quantitating a polypeptide in tissue, as molecular weight markers and as
 CC a food supplement. (II) and its binding partners are useful in medical
 CC imaging of sites expressing (II). (I) and (II) are useful for treating
 CC disorders involving aberrant protein expression or biological activity.
 CC The polypeptide and polynucleotide sequences have applications in
 CC diagnostics, forensics, gene mapping, identification of mutations
 CC responsible for genetic disorders or other traits to assess biodiversity
 CC and to produce other types of data and products dependent on DNA and
 CC amino acid sequences. ABG0010-ABG3037 represent novel human
 CC diagnostic amino acid sequences of the invention.
 CC Note: The sequence data for this patent did not appear in the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequences.

XX Sequence 543 AA;

XX Query Match 23.6%; Score 319.5; DB 22; Length 543;

XX Best Local Similarity 29.3%; Pred. No. 8.9e-24;

XX Matches 93; Conservative 45; Mismatches 112; Indels 67; Gaps 9;

QY 2 GSPSRKSLSPSSSSV-----QCGGYTMEARSKATAVAGSPGAG 46
 DB 33 GAEPITVSPSPSSAKGAVNFSSLSMTPEGSSGCVTPFGGASSFSVPSYPAGLTGG 92
 QY 47 -----GPAELSLRLEGEPLITVSE-DGDMWTVLSEVSGREYIPSVHAKV-- 90
 DB 93 VTIFVALYDEARTEDTDLSPFKSGERPIINNEGDMWEARSIATGKNGYIPSNVYAPADS 152
 QY 91 ---SHGWLVEGLSREKAEELLPGNPGCAFILRESQTRGSGYSVLRSPASMDRIR-- 146
 DB 153 IOAEWYFCKMKRKAERLLNPGNORGILVRESEITKGVSLSTR-----DMDELNGD 207
 QY 147 ---HYRIHLDNGMLYISPRITPSSIOALVDHYSIELADDTICLKEPC-----VLQ 194
 DB 208 NVKHYKRIKLDNGCYITTRAGQFTLQKLVKHYTHEADGICLHKLTVCPYVAPQTOGLAK 267
 QY 195 RAGPLFGKDIPLPYVQV-----TPLNKELDSSLSEEAATGEESLSEGL 240
 DB 266 DAMEIPRESLRLEVYLGCGCEGYVMGTWNGTTKVAITKLKPGTMMPEAFLOEQIMKKL 327
 QY 241 LRESL-SFYISLNDNAV 256
 DB 328 RHDKLVPLVAVVSEPI 344

RESULT 14

AAB84663

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Page 10

CC may be used to assay for agents which modulate SFK expression and activity or as antigens in the production of antibodies against SFK. The CC proteins may also be administered to a patient to rectify inappropriate, or low levels of, SFK expression in a patient.

50 Sequence 496 AA;

Query Match

23.58; Score 317.5; DB 20; Length 496;
26.09; Prod No 1 30-33;

Matches 7

34; Mismatches 74; Indels 27; Gaps 6;

QY 1 MGS 11

LPSPSLSSVQGGP---VTM-EAERS-----KATAVALG 41

Db 1 MGC

LGPRSTQTHYVKDPTSTVTMTKPERSSKHPRREGQEEVLLALY 600

QY 42 SEP

EP L T V S E D G D W W T V L S E V S G R E Y N I P S V H V A K V - - - S H G W L Y E 97

Db 61 DYD

DHL LKESGEWEACLISTGEEGVPSNYVAYFNSLESEEWYFK 12

QY	98	GLS	1:1
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NPGGAELRESQTRRGSSLSVRLSRPASWDRIKHYRIHCLDNCW 13
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121 6MS

NNSGAEMLKROSEIMKGCFSLSVR ---DSGDI VVHIAIRILEDSG 1/

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